Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2017/08/09 13:02:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/bethany/projects/planctomycetes+halococci/QC/Gem_JW9.sorted.ba
m -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	blasr /home/bethany/projects/planctomycetes/pacbio_raw/Jw9/Analysis_Results/m160619_212717_42244_c101005612550000001823230309161615_s1_p0.bas.h5 /home/bethany/projects/planctomycetes/assembly/final_contigs/Gem_JW9_final_contigs.fasta --sam --nproc 16 --out Gem_JW9.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	1 (5.3.574e1c2)
Analysis date:	Wed Aug 09 12:59:29 NZST 2017
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/bethany/projects/planctomycetes+halococci/QC/Gem_JW9.sorted.bam

2. Summary

2.1. Globals

Reference size	10,038,093
Number of reads	202,374
Mapped reads	202,374 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	48 / 40,281 / 8,769.3
Duplicated reads (estimated)	32,418 / 16.02%
Duplication rate	6.66%
Clipped reads	202,371 / 100%

2.2. ACGT Content

Number/percentage of A's	169,742,361 / 18.29%
Number/percentage of C's	286,843,923 / 30.9%
Number/percentage of T's	168,869,656 / 18.19%
Number/percentage of G's	286,259,392 / 30.84%
Number/percentage of N's	0 / 0%
GC Percentage	61.74%

2.3. Coverage

Mean	96.3335
Standard Deviation	31.9984

2.4. Mapping Quality

Mean Mapping Quality	225.36

2.5. Mismatches and indels

| General error rate	16.22%
Insertions	72,887,286
Mapped reads with at least one insertion	99.74%
Deletions	35,217,443
Mapped reads with at least one deletion	99.19%
Homopolymer indels	18.28%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
contig01	3362574	329129348	97.8802	36.0532
contig02	6619391	627897952	94.8574	28.8928
contig03	56128	9977499	177.7633	18.2532

3. Results : Coverage across reference

Coverage across reference
Gem_JW9.sorted.bam

4. Results : Coverage Histogram

Coverage Histogram
Gem_JW9.sorted.bam
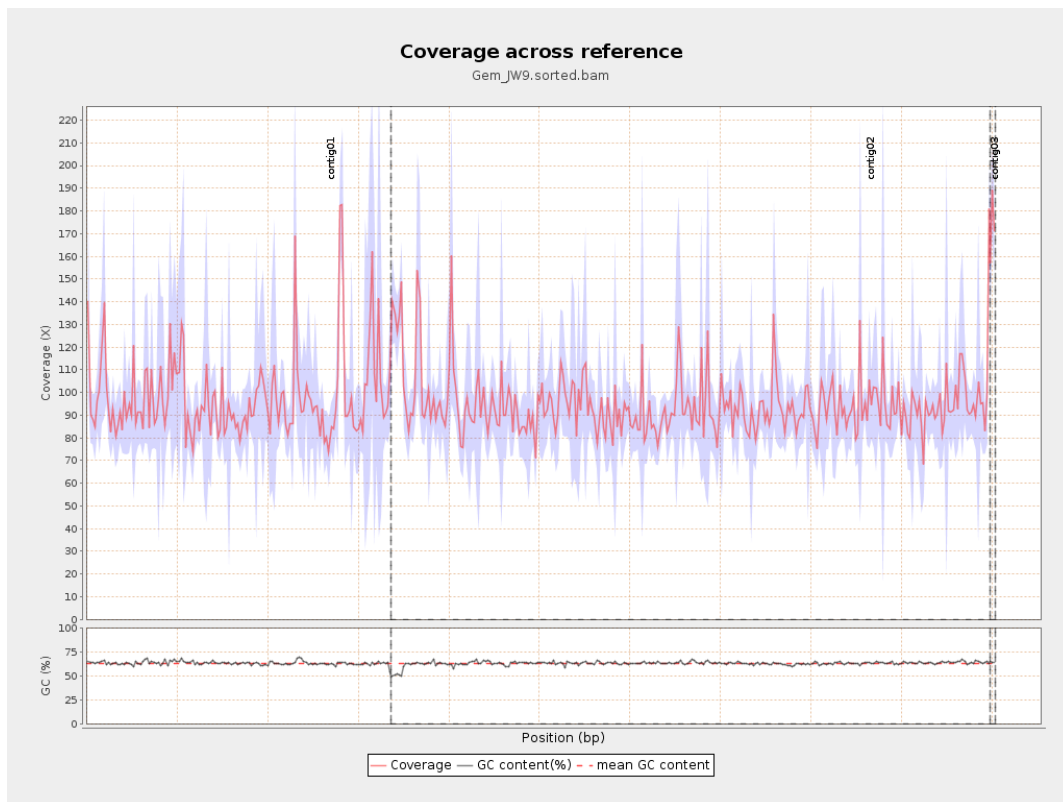
5. Results : Coverage Histogram (0-50X)
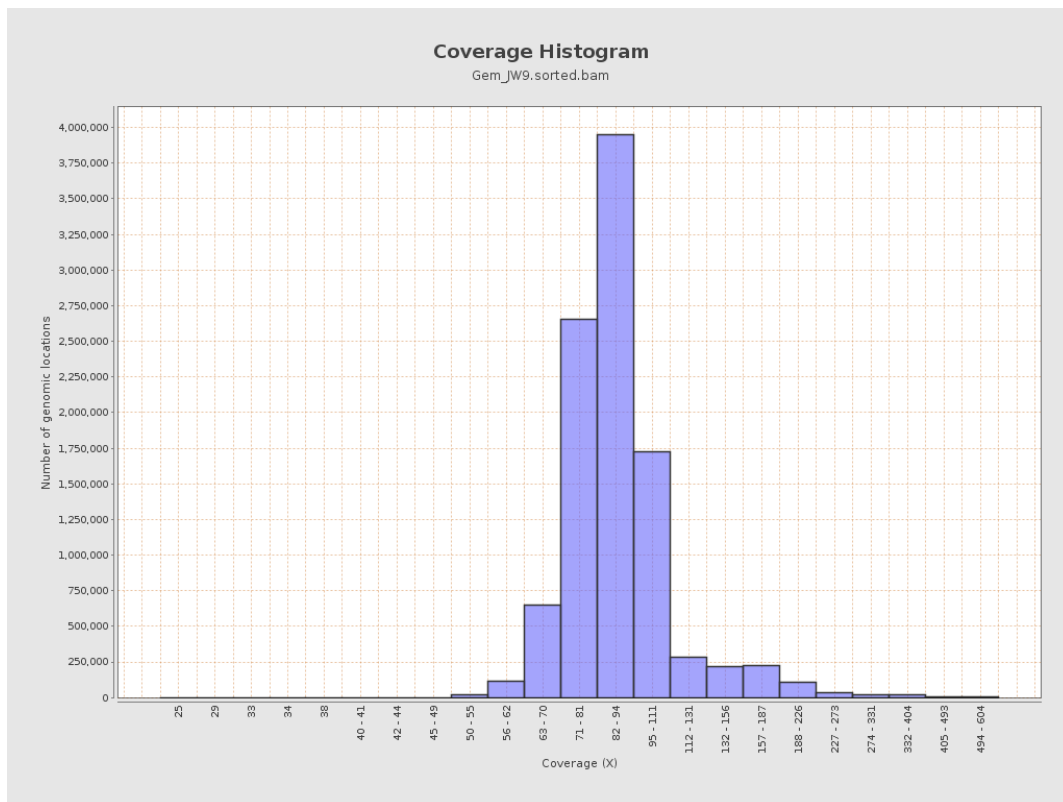
Coverage Histogram (0-50X)
Gem_JW9.sorted.bam
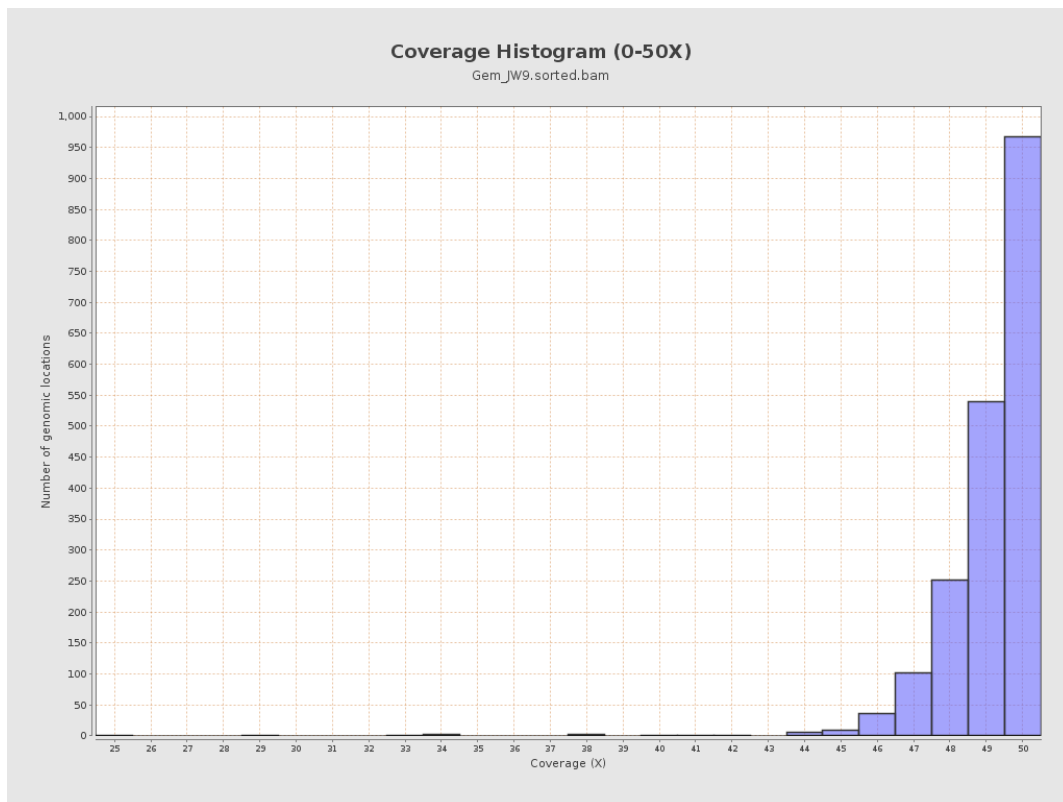
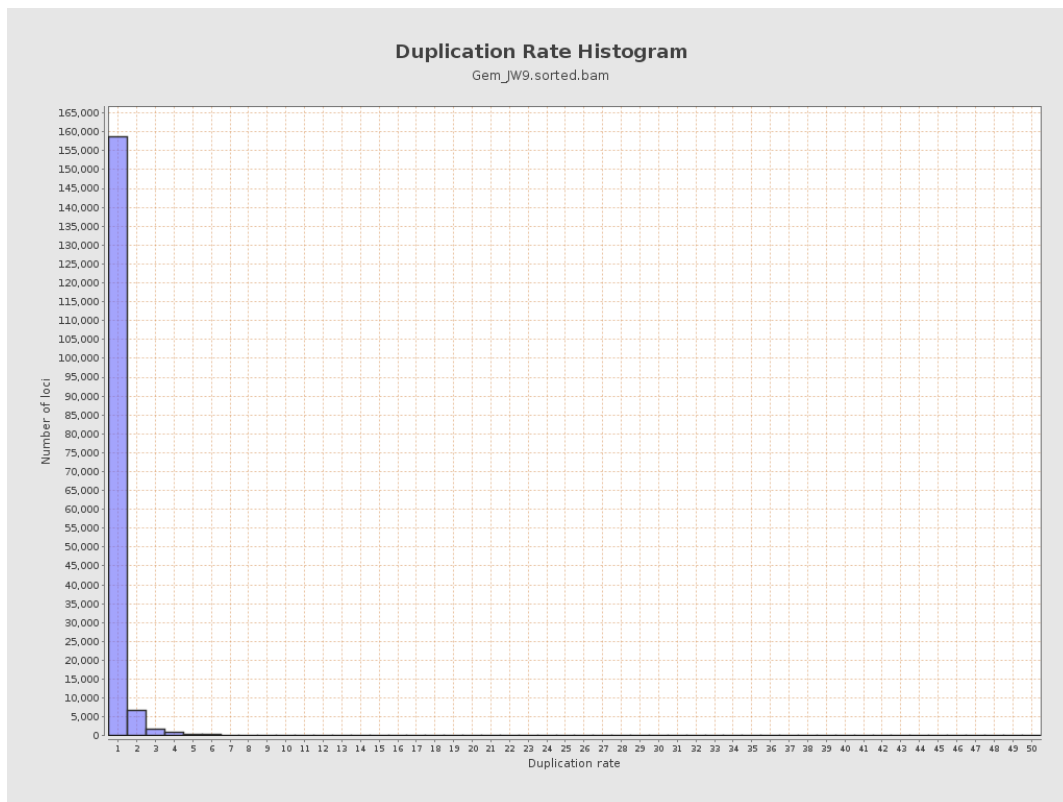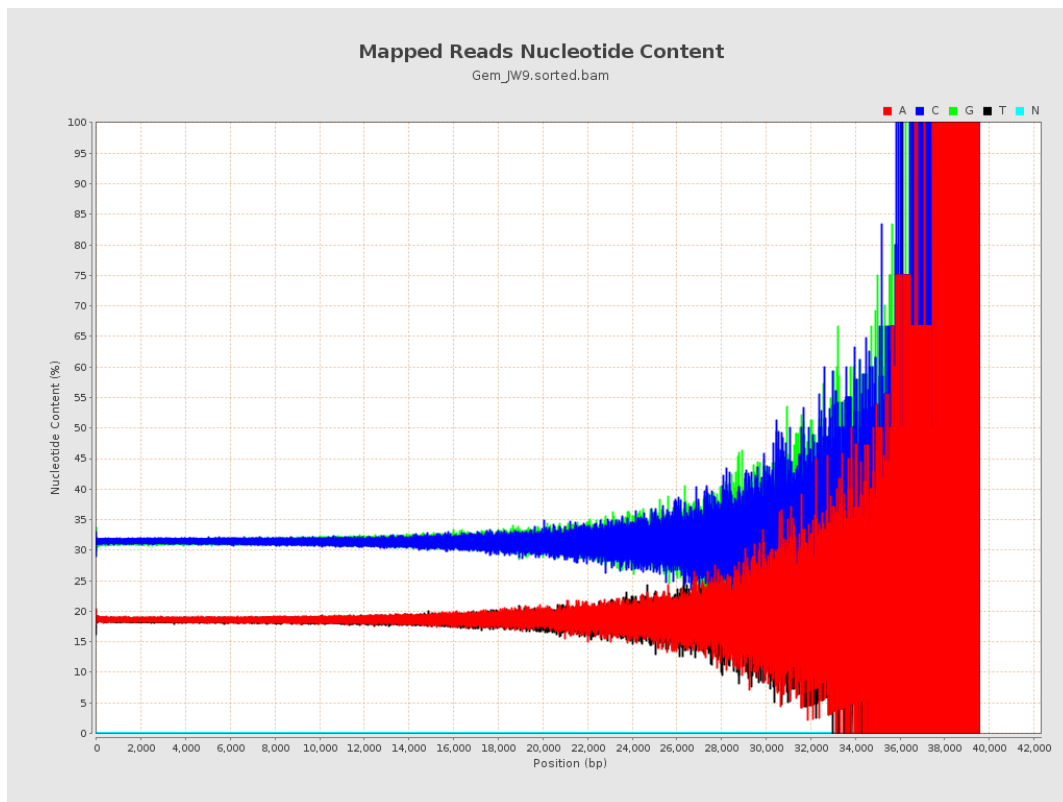# 6. Results : Genome Fraction Coverage
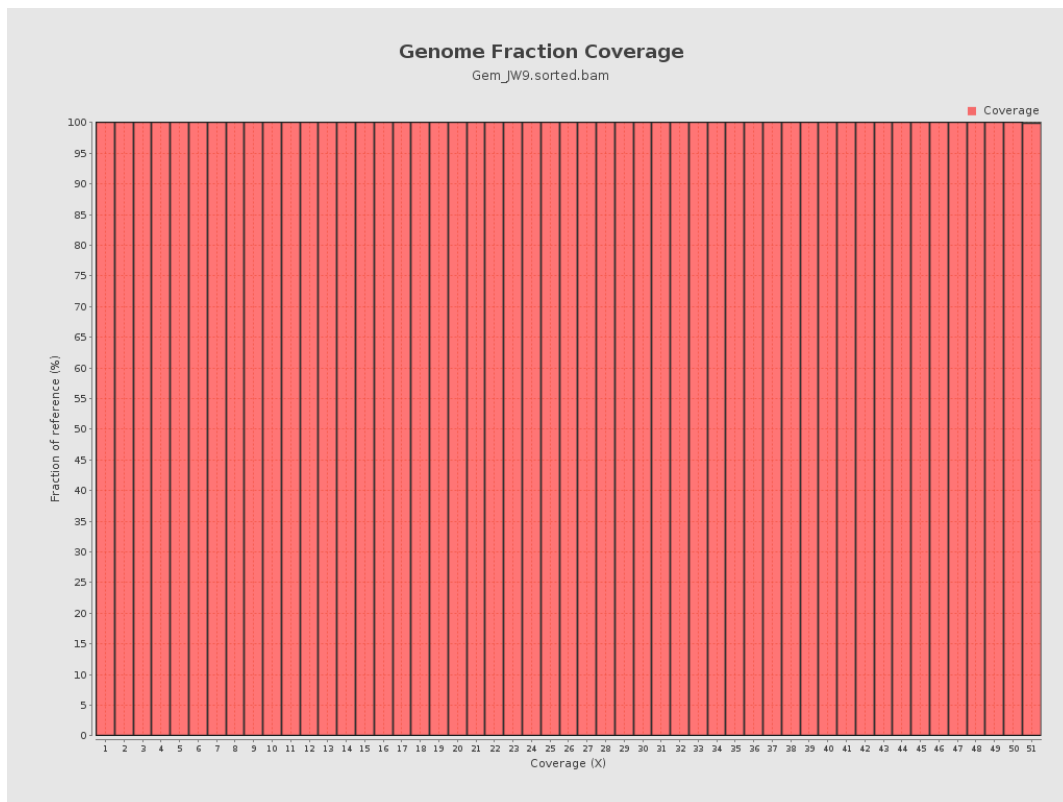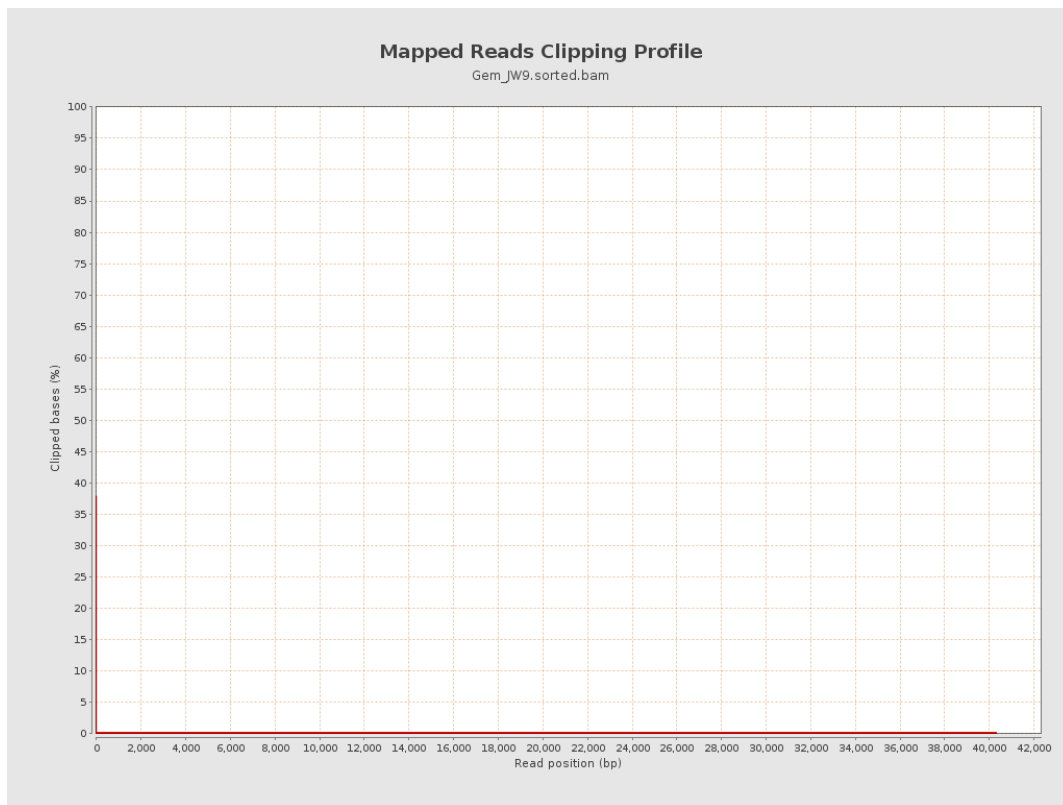
7. Results : Duplication Rate Histogram

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
Gem_JW9.sorted.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
Gem_JW9.sorted.bam
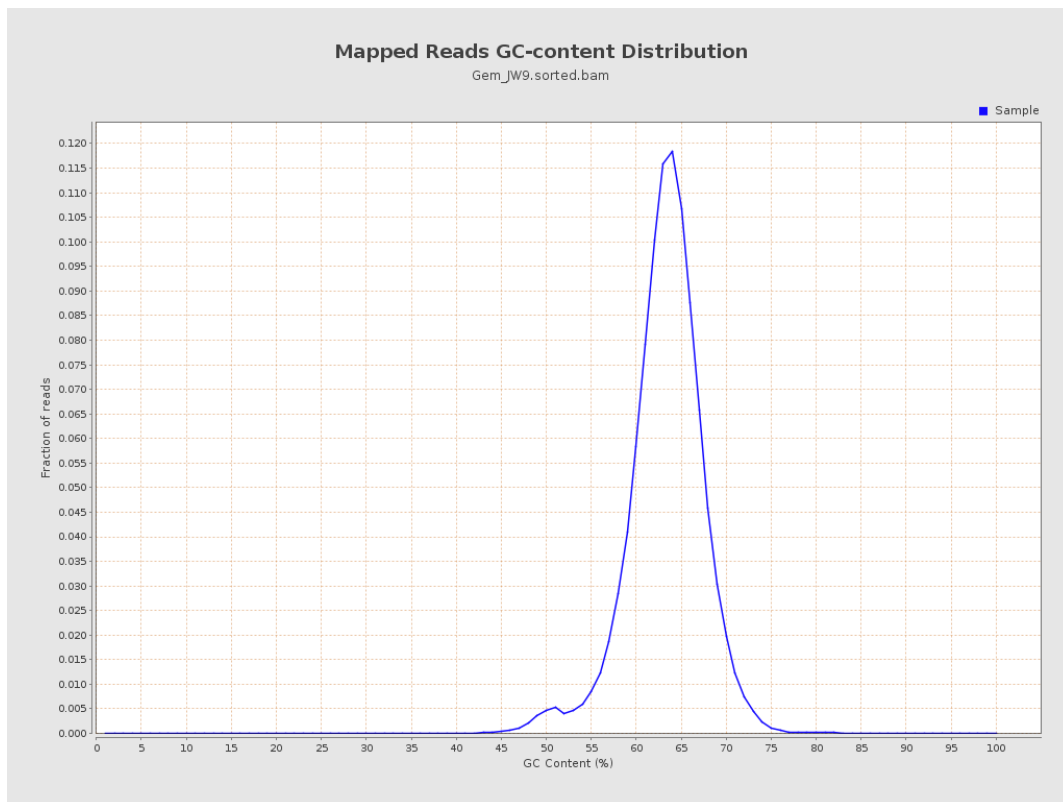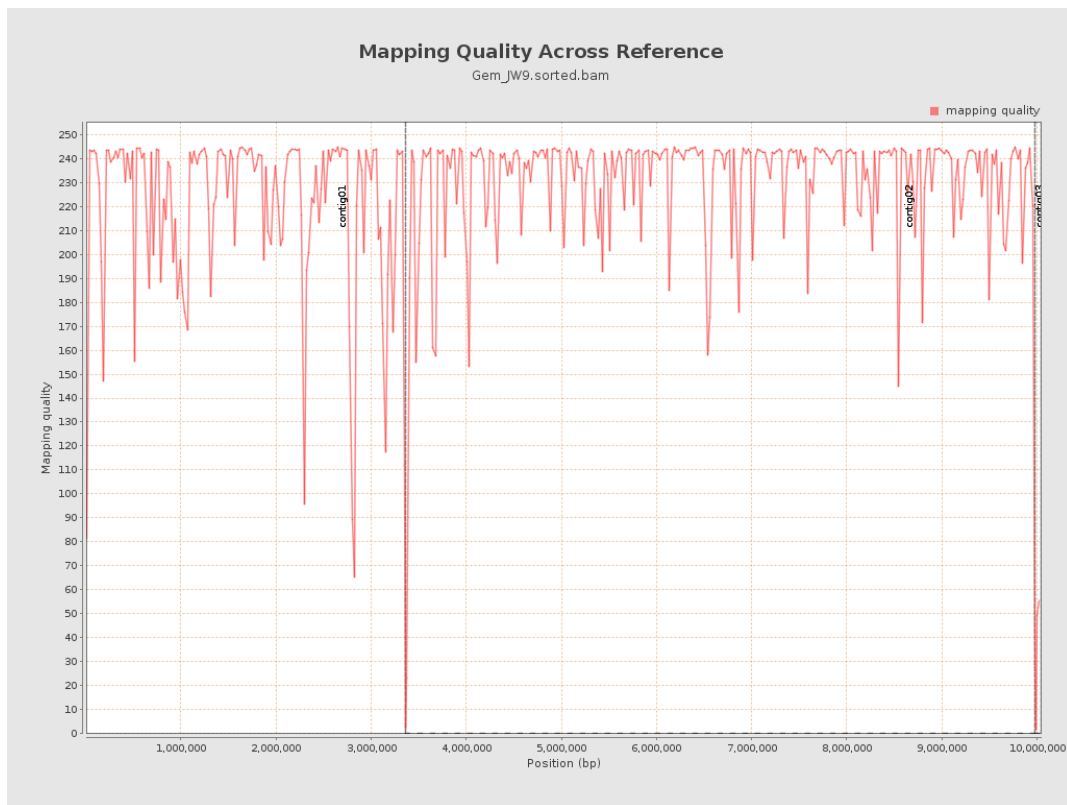
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
Gem_JW9.sorted.bam

11. Results : Homopolymer Indels
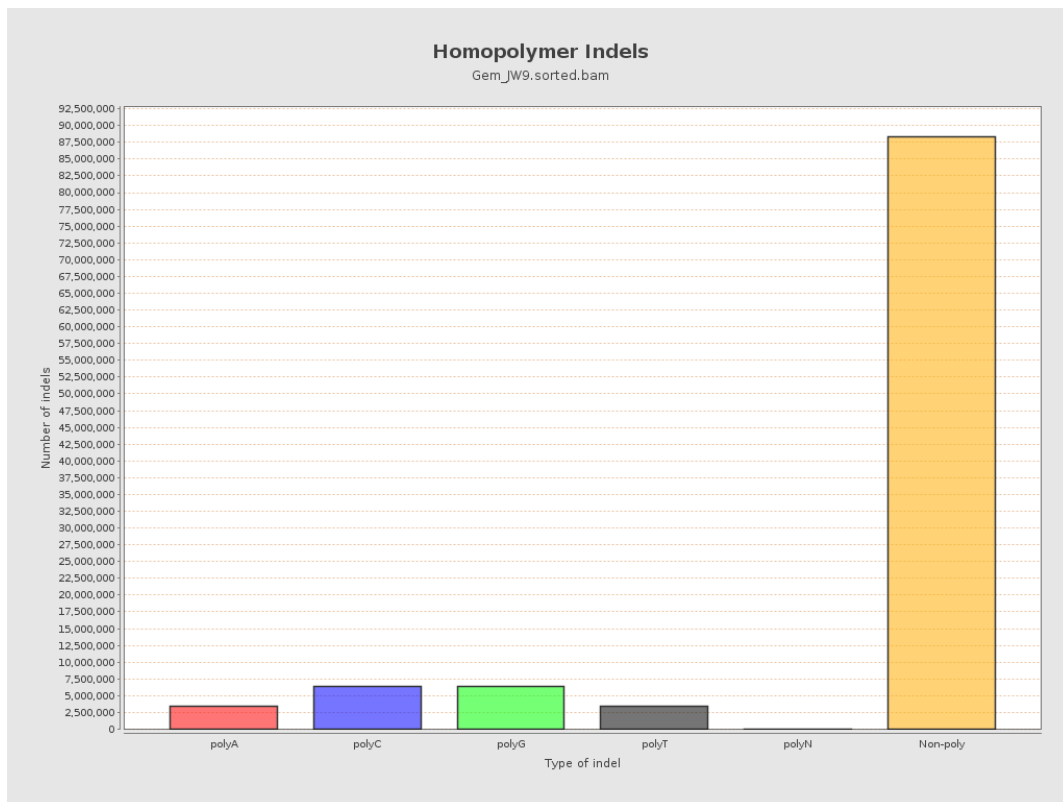
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram